STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 100793

TO: Maury Audet
Location: CM1/11D04/11D13
Art Unit: 1645
Monday, August 18, 2003

Case Serial Number: 09/846779

From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

Dear Examiner:

Please see attached results.

Feel free to contact me if you have any questions.

Thank you for using STIC services

Mona Smith
308-3278

STIC-Biotech/ChemLib

10/846,793

From: STIC-ILL
Sent: Monday, August 11, 2003 6:45 AM
To: STIC-Biotech/ChemLib
Subject: FW: Search of SEQ ID NO: 1 (09/846,779)

-----Original Message-----
From: Audet, Maury
Sent: Sunday, August 10, 2003 3:06 PM
To: STIC-ILL
Subject: Search of SEQ ID NO: 1 (09/846,779)

Please search SEQ ID NO: 1 for Ser. No. 09/846,779 (including interfer. files RAPM, RAPN).
Thanks, Maury

Maury Audet
Patent Examiner
Art Unit 1654
703-305-5039
11D04

Searcher: M. Smith
Phone:
Location:
Date Picked Up: 8/11/03
Date Completed: 8/18/03
Searcher Prep/Review: 3
Clerical: 5
Online time: 5

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 1
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2003, 23:53:08 ; Search time 69 Seconds
(without alignments)
29.905 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	13	18	AAW22856	Human serum amyloi
2	77	100.0	13	22	AAB90433	Human SAA amino tr
3	77	100.0	13	22	AAB90534	Human SAA internal
4	77	100.0	14	22	AAB90432	Human SAA amino tr
5	77	100.0	14	22	AAB90533	Human SAA internal
6	77	100.0	15	22	AAB90431	Human SAA amino tr
7	77	100.0	15	22	AAB90532	Human SAA internal
8	77	100.0	16	22	AAB90430	Human SAA amino tr
9	77	100.0	16	22	AAB90531	Human SAA internal
10	77	100.0	17	22	AAB90429	Human SAA amino tr
11	77	100.0	17	22	AAB90530	Human SAA internal
12	77	100.0	18	22	AAB90428	Human SAA amino tr
13	77	100.0	18	22	AAB90529	Human SAA internal
14	77	100.0	19	22	AAB90427	Human SAA amino tr
15	77	100.0	19	22	AAB90528	Human SAA internal
16	77	100.0	20	22	AAB90426	Human SAA amino tr
17	77	100.0	20	22	AAB90527	Human SAA internal
18	77	100.0	21	22	AAB90425	Human SAA amino tr
19	77	100.0	21	22	AAB90526	Human SAA internal
20	77	100.0	22	22	AAB90424	Human SAA amino tr
21	77	100.0	22	22	AAB90525	Human SAA internal
22	77	100.0	23	22	AAB90423	Human SAA amino tr
23	77	100.0	23	22	AAB90524	Human SAA internal
24	77	100.0	24	22	AAB90422	Human SAA amino tr
25	77	100.0	24	22	AAB90523	Human SAA internal
26	77	100.0	25	22	AAB90421	Human SAA amino tr
27	77	100.0	25	22	AAB90522	Human SAA internal
28	77	100.0	26	22	AAB90420	Human SAA amino tr
29	77	100.0	26	22	AAB90521	Human SAA internal
30	77	100.0	27	22	AAB90419	Human SAA amino tr
31	77	100.0	27	22	AAB90520	Human SAA internal
32	77	100.0	28	22	AAB90418	Human SAA amino tr
33	77	100.0	28	22	AAB90519	Human SAA internal
34	77	100.0	29	22	AAB90417	Human SAA amino tr
35	77	100.0	29	22	AAB90518	Human SAA internal
36	77	100.0	30	22	AAB90416	Human SAA amino tr
37	77	100.0	30	22	AAB90517	Human SAA internal
38	77	100.0	31	22	AAB90415	Human SAA amino tr
39	77	100.0	31	22	AAB90516	Human SAA internal
40	77	100.0	32	22	AAB90414	Human SAA amino tr
41	77	100.0	32	22	AAB90515	Human SAA internal
42	77	100.0	33	22	AAB90413	Human SAA amino tr
43	77	100.0	33	22	AAB90514	Human SAA internal
44	77	100.0	34	22	AAB90412	Human SAA amino tr
45	77	100.0	34	22	AAB90513	Human SAA internal

ALIGNMENTS

RESULT 1
AAW22856
ID AAW22856 standard; peptide; 13 AA.
XX
AC AAW22856;
XX
DT 18-SEP-1997 (first entry)
XX
DE Human serum amyloid A antigen peptide fragment.
XX
KW Serum amyloid A; SAA; antigen; antibody; monoclonal; hybridoma;
KW blood.
XX
OS Homo sapiens.
XX
PN JP09121888-A.
XX
PD 13-MAY-1997.
XX
PF 06-NOV-1995; 95JP-0311531.
XX
PR 06-NOV-1995; 95JP-0311531.
XX
PA (MAZN) COSMO OIL CO LTD.
PA (COSM-) COSMO SOGO KENKYUSHO KK.
XX
DR WPI; 1997-314238/29.
XX
PT Monoclonal antibody specific for human serum amyloid A (SAA) antigen
PT - used for selective determination of SAA1 and SAA1 des-Arginine in
PT human blood
XX

PS Example 3; Page 10; 12pp; Japanese.
XX
CC AAW22854-58 are peptide fragments of human serum amyloid A (SAA) antigen. The peptides were used to test the selectivity of a new monoclonal antibody (SAA03-6) which specifically binds to human serum amyloid A antigens SAA1 and SAA1 desArg but does not bind to SAA2 alpha, SAA2 alpha-desArg, SAA2 beta and SAA2 beta-desArg. The antibody is used for selectively determining the total amount of SAA1 and SAA1 desArg in human blood.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 77; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
|||||||||||||
Db 1 PNHFRPAGLPEKY 13

RESULT 2
AAB90433
ID AAB90433 standard; Peptide; 13 AA.
XX
AC AAB90433;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA amino truncation, SEQ ID NO: 191.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 22; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 77; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
|||||||||||||
Db 1 PNHFRPAGLPEKY 13

RESULT 3 SAME AS 2
AAB90534
ID AAB90534 standard; Peptide; 13 AA.
XX
AC AAB90534;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA internal truncation, SEQ ID NO: 292.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 34; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 77; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
|||||||||||||
Db 1 PNHFRPAGLPEKY 13

RESULT 4
AAB90432
ID AAB90432 standard; Peptide; 14 AA.
XX
AC AAB90432;

XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA amino truncation, SEQ ID NO: 190.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 22; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 77; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||| |
Db 2 PNHFRPAGLPEKY 14

RESULT 5
AAB90533
ID AAB90533 standard; Peptide; 14 AA.
XX
AC AAB90533;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA internal truncation, SEQ ID NO: 291.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 34; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 77; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||| |
Db 2 PNHFRPAGLPEKY 14

RESULT 6
AAB90431
ID AAB90431 standard; Peptide; 15 AA.
XX
AC AAB90431;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA amino truncation, SEQ ID NO: 189.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.

```
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 22; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   15 AA;

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Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          3 PNHFRPAGLPEKY 15


RESULT 7
AAB90532
ID   AAB90532 standard; Peptide; 15 AA.
XX
AC   AAB90532;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA internal truncation, SEQ ID NO: 290.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
 )   29-MAR-2001.
.X
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 34; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 22;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          3 PNHFRPAGLPEKY 15


RESULT 8
AAB90430
ID   AAB90430 standard; Peptide; 16 AA.
XX
AC   AAB90430;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA amino truncation, SEQ ID NO: 188.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 22; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   16 AA;

  Query Match             100.0%;  Score 77;  DB 22;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
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```
Db          4 PNHFRPAGLPEKY 16


RESULT 9
AAB90531
ID   AAB90531 standard; Peptide; 16 AA.
XX
AC   AAB90531;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA internal truncation, SEQ ID NO: 289.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 34; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   16 AA;

  Query Match             100.0%;  Score 77;  DB 22;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          4 PNHFRPAGLPEKY 16


RESULT 10
AAB90429
ID   AAB90429 standard; Peptide; 17 AA.
XX
AC   AAB90429;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA amino truncation, SEQ ID NO: 187.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 22; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   17 AA;

  Query Match             100.0%;  Score 77;  DB 22;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          5 PNHFRPAGLPEKY 17


RESULT 11
AAB90530
ID   AAB90530 standard; Peptide; 17 AA.
XX
AC   AAB90530;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA internal truncation, SEQ ID NO: 288.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
```

XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 34; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 77; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||
Db 5 PNHFRPAGLPEKY 17

RESULT 12
AAB90428
ID AAB90428 standard; Peptide; 18 AA.
XX
AC AAB90428;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA amino truncation, SEQ ID NO: 186.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 22; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 77; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||
Db 6 PNHFRPAGLPEKY 18

RESULT 13
AAB90529
ID AAB90529 standard; Peptide; 18 AA.
XX
AC AAB90529;
XX
DT 01-JUN-2001 (first entry)
XX
DE Human SAA internal truncation, SEQ ID NO: 287.
XX
KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121188-A1.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-1999; 99WO-US21770.
XX
PR 22-SEP-1999; 99WO-US21770.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
DR WPI; 2001-211457/21.
XX
PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX
PS Disclosure; Page 34; 141pp; English.
XX
CC The present sequence is a fragment of human serum amyloid A (SAA). The
CC invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPRL1. Modulators
CC of the SAA/FPRL1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPRL1 complex.
XX

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SQ   Sequence   18 AA;

  Query Match            100.0%;  Score 77;  DB 22;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          6 PNHFRPAGLPEKY 18


RESULT 14
AAB90427
ID   AAB90427 standard; Peptide; 19 AA.
XX
AC   AAB90427;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA amino truncation, SEQ ID NO: 185.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 22; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   19 AA;

  Query Match            100.0%;  Score 77;  DB 22;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          7 PNHFRPAGLPEKY 19


RESULT 15
AAB90528
ID   AAB90528 standard; Peptide; 19 AA.
XX
AC   AAB90528;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human SAA internal truncation, SEQ ID NO: 286.
XX
KW   Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW   antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
KW   immune system disorder; amyloidosis; inflammation; infection;
KW   organ rejection; arthritis; atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200121188-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-1999;   99WO-US21770.
XX
PR   22-SEP-1999;   99WO-US21770.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang J,  Oppenheim JJ,  Su S,  Gong W,  Gao J,  Murphy PM;
XX
DR   WPI; 2001-211457/21.
XX
PT   New serum amyloid A and formyl peptide receptor variant complex and its
PT   modulators, useful for treating immune system disorders, amyloidosis,
PT   inflammation, infection, organ rejection, arthritis, atherosclerosis
PT   and neoplasia -
XX
PS   Disclosure; Page 33; 141pp; English.
XX
CC   The present sequence is a fragment of human serum amyloid A (SAA). The
CC   invention relates to the discovery that SAA is a ligand for FPRL1 (human
CC   formyl peptide receptor variant). A complex has been isolated that
CC   comprises a peptide agent with a sequence corresponding to SAA, or its
CC   conservative variant or functional fragment, bound to FPRL1. Modulators
CC   of the SAA/FPRL1 complex are useful for treating immune system
CC   disorders, amyloidosis, inflammation, infection, organ rejection,
CC   arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC   for their ability to modulate assembly of the SAA/FPRL1 complex.
XX
SQ   Sequence   19 AA;

  Query Match            100.0%;  Score 77;  DB 22;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          7 PNHFRPAGLPEKY 19


Search completed: August 18, 2003, 01:24:05
Job time : 69 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2003, 01:26:28 ; Search time 52 Seconds
(without alignments)
32.751 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	13	15	US-10-099-782A-191	Sequence 191, App
2	77	100.0	13	15	US-10-099-782A-292	Sequence 292, App
3	77	100.0	14	15	US-10-099-782A-190	Sequence 190, App
4	77	100.0	14	15	US-10-099-782A-291	Sequence 291, App
5	77	100.0	15	15	US-10-099-782A-189	Sequence 189, App
6	77	100.0	15	15	US-10-099-782A-290	Sequence 290, App
7	77	100.0	16	15	US-10-099-782A-188	Sequence 188, App
8	77	100.0	16	15	US-10-099-782A-289	Sequence 289, App
9	77	100.0	17	15	US-10-099-782A-187	Sequence 187, App
10	77	100.0	17	15	US-10-099-782A-288	Sequence 288, App
11	77	100.0	18	15	US-10-099-782A-186	Sequence 186, App
12	77	100.0	18	15	US-10-099-782A-287	Sequence 287, App
13	77	100.0	19	15	US-10-099-782A-185	Sequence 185, App
14	77	100.0	19	15	US-10-099-782A-286	Sequence 286, App
15	77	100.0	20	15	US-10-099-782A-184	Sequence 184, App
16	77	100.0	20	15	US-10-099-782A-285	Sequence 285, App
17	77	100.0	21	15	US-10-099-782A-183	Sequence 183, App
18	77	100.0	21	15	US-10-099-782A-284	Sequence 284, App
19	77	100.0	22	15	US-10-099-782A-182	Sequence 182, App
20	77	100.0	22	15	US-10-099-782A-283	Sequence 283, App
21	77	100.0	23	15	US-10-099-782A-181	Sequence 181, App
22	77	100.0	23	15	US-10-099-782A-282	Sequence 282, App
23	77	100.0	24	15	US-10-099-782A-180	Sequence 180, App
24	77	100.0	24	15	US-10-099-782A-281	Sequence 281, App
25	77	100.0	25	15	US-10-099-782A-179	Sequence 179, App
26	77	100.0	25	15	US-10-099-782A-280	Sequence 280, App
27	77	100.0	26	15	US-10-099-782A-178	Sequence 178, App
28	77	100.0	26	15	US-10-099-782A-279	Sequence 279, App
29	77	100.0	27	15	US-10-099-782A-177	Sequence 177, App
30	77	100.0	27	15	US-10-099-782A-278	Sequence 278, App
31	77	100.0	28	15	US-10-099-782A-176	Sequence 176, App
32	77	100.0	28	15	US-10-099-782A-277	Sequence 277, App
33	77	100.0	29	15	US-10-099-782A-175	Sequence 175, App
34	77	100.0	29	15	US-10-099-782A-276	Sequence 276, App
35	77	100.0	30	15	US-10-099-782A-174	Sequence 174, App
36	77	100.0	30	15	US-10-099-782A-275	Sequence 275, App
37	77	100.0	31	15	US-10-099-782A-173	Sequence 173, App
38	77	100.0	31	15	US-10-099-782A-274	Sequence 274, App
39	77	100.0	32	15	US-10-099-782A-172	Sequence 172, App
40	77	100.0	32	15	US-10-099-782A-273	Sequence 273, App
41	77	100.0	33	15	US-10-099-782A-171	Sequence 171, App
42	77	100.0	33	15	US-10-099-782A-272	Sequence 272, App
43	77	100.0	34	15	US-10-099-782A-170	Sequence 170, App
44	77	100.0	34	15	US-10-099-782A-271	Sequence 271, App
45	77	100.0	35	15	US-10-099-782A-169	Sequence 169, App

ALIGNMENTS

RESULT 1
US-10-099-782A-191
; Sequence 191, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-191

Query Match 100.0%; Score 77; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||||
Db 1 PNHFRPAGLPEKY 13

RESULT 2
US-10-099-782A-292
; Sequence 292, Application US/10099782A

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;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-288

  Query Match             100.0%;  Score 77;  DB 15;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          5 PNHFRPAGLPEKY 17


RESULT 11
US-10-099-782A-186
; Sequence 186, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
;  APPLICANT: Ji-Ming Wang
;  APPLICANT:  Joost J. Oppenheim
;  APPLICANT:  Shao-Bo Su
;  APPLICANT:  Wang-Hua Gong
;  APPLICANT:  Ji-Liang Gao
;  APPLICANT:  Philip M. Murphy
;  TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
;  TITLE OF INVENTION:  RECEPTOR BY SERUM AMYLOID A (SAA)
;  FILE REFERENCE: NIH173.001C1
;  CURRENT APPLICATION NUMBER: US/10/099,782A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-186

  Query Match             100.0%;  Score 77;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
;
Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          6 PNHFRPAGLPEKY 18


RESULT 12
US-10-099-782A-287
; Sequence 287, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
;  APPLICANT: Ji-Ming Wang
;  APPLICANT:  Joost J. Oppenheim
;  APPLICANT:  Shao-Bo Su
;  APPLICANT:  Wang-Hua Gong
;  APPLICANT:  Ji-Liang Gao
;  APPLICANT:  Philip M. Murphy
;  TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
;  TITLE OF INVENTION:  RECEPTOR BY SERUM AMYLOID A (SAA)
;  FILE REFERENCE: NIH173.001C1
;  CURRENT APPLICATION NUMBER: US/10/099,782A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 287
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-287

  Query Match             100.0%;  Score 77;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          6 PNHFRPAGLPEKY 18


RESULT 13
US-10-099-782A-185
; Sequence 185, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
;  APPLICANT: Ji-Ming Wang
;  APPLICANT:  Joost J. Oppenheim
;  APPLICANT:  Shao-Bo Su
;  APPLICANT:  Wang-Hua Gong
;  APPLICANT:  Ji-Liang Gao
;  APPLICANT:  Philip M. Murphy
;  TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
;  TITLE OF INVENTION:  RECEPTOR BY SERUM AMYLOID A (SAA)
;  FILE REFERENCE: NIH173.001C1
;  CURRENT APPLICATION NUMBER: US/10/099,782A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-185

  Query Match             100.0%;  Score 77;  DB 15;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          7 PNHFRPAGLPEKY 19


RESULT 14
US-10-099-782A-286
; Sequence 286, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
;  APPLICANT: Ji-Ming Wang
;  APPLICANT:  Joost J. Oppenheim
;  APPLICANT:  Shao-Bo Su
;  APPLICANT:  Wang-Hua Gong
;  APPLICANT:  Ji-Liang Gao
;  APPLICANT:  Philip M. Murphy
;  TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
;  TITLE OF INVENTION:  RECEPTOR BY SERUM AMYLOID A (SAA)
;  FILE REFERENCE: NIH173.001C1
;  CURRENT APPLICATION NUMBER: US/10/099,782A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 286
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;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-286

  Query Match            100.0%;  Score 77;  DB 15;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 6.4e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          7 PNHFRPAGLPEKY 19


RESULT 15
US-10-099-782A-184
; Sequence 184, Application US/10099782A
; Publication No. US20030120037A1
; GENERAL INFORMATION:
;  APPLICANT: Ji-Ming Wang
;  APPLICANT:  Joost J. Oppenheim
;  APPLICANT:  Shao-Bo Su
;  APPLICANT:  Wang-Hua Gong
;  APPLICANT:  Ji-Liang Gao
;  APPLICANT:  Philip M. Murphy
;  TITLE OF INVENTION: UTILIZATION OF FPRL1 AS A FUNCTIONAL
;  TITLE OF INVENTION:  RECEPTOR BY SERUM AMYLOID A (SAA)
;  FILE REFERENCE: NIH173.001C1
;  CURRENT APPLICATION NUMBER: US/10/099,782A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US99/21770
;  PRIOR FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 301
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 184
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-099-782A-184

  Query Match            100.0%;  Score 77;  DB 15;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db          8 PNHFRPAGLPEKY 20


Search completed: August 18, 2003, 01:34:56
Job time : 52 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2003, 01:22:53 ; Search time 42 Seconds
(without alignments)
13.096 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	122	4	US-09-154-750A-82	Sequence 82, Appl
2	71	92.2	129	4	US-09-425-679E-11	Sequence 11, Appl
3	68	88.3	17	4	US-09-425-679E-8	Sequence 8, Appli
4	68	88.3	104	4	US-09-029-345-1	Sequence 1, Appli
5	68	88.3	110	4	US-09-425-679E-10	Sequence 10, Appl
6	45	58.4	112	3	US-09-240-274-64	Sequence 64, Appl
7	42	54.5	845	4	US-09-252-991A-17856	Sequence 17856, A
8	40	51.9	109	3	US-09-240-274-61	Sequence 61, Appl
9	40	51.9	363	4	US-09-252-991A-19920	Sequence 19920, A
10	40	51.9	497	4	US-09-252-991A-23620	Sequence 23620, A
11	40	51.9	762	4	US-09-252-991A-29423	Sequence 29423, A
12	39	50.6	109	2	US-08-672-345C-3	Sequence 3, Appli
13	39	50.6	109	2	US-08-672-345C-93	Sequence 93, Appl
14	39	50.6	109	3	US-09-214-095D-3	Sequence 3, Appli
15	39	50.6	109	3	US-09-214-095D-121	Sequence 121, App
16	39	50.6	111	3	US-08-983-607-35	Sequence 35, Appl
17	39	50.6	112	3	US-08-983-607-31	Sequence 31, Appl
18	39	50.6	112	3	US-08-983-607-49	Sequence 49, Appl
19	39	50.6	114	3	US-09-240-274-62	Sequence 62, Appl
20	39	50.6	123	4	US-09-996-243-117	Sequence 117, App
21	39	50.6	132	2	US-08-345-321-4	Sequence 4, Appli
22	39	50.6	181	4	US-09-252-991A-23085	Sequence 23085, A
23	39	50.6	234	4	US-09-372-425A-4	Sequence 4, Appli
24	39	50.6	503	4	US-09-252-991A-32663	Sequence 32663, A
25	39	50.6	680	1	US-08-211-430-2	Sequence 2, Appli
26	39	50.6	680	3	US-08-761-136-1	Sequence 1, Appli
27	39	50.6	680	4	US-09-576-967-1	Sequence 1, Appli
28	38	49.4	98	1	US-08-211-202-111	Sequence 111, App
29	38	49.4	98	2	US-08-665-202-38	Sequence 38, Appl
30	38	49.4	98	4	US-09-315-574-38	Sequence 38, Appl
31	38	49.4	106	1	US-08-259-372A-16	Sequence 16, Appl
32	38	49.4	106	1	US-08-468-671-16	Sequence 16, Appl
33	38	49.4	107	4	US-09-025-769B-34	Sequence 34, Appl
34	38	49.4	107	4	US-09-025-769B-55	Sequence 55, Appl
35	38	49.4	108	1	US-08-360-125-12	Sequence 12, Appl
36	38	49.4	108	2	US-08-450-578-12	Sequence 12, Appl
37	38	49.4	108	2	US-09-017-628-12	Sequence 12, Appl
38	38	49.4	108	2	US-09-014-880-12	Sequence 12, Appl
39	38	49.4	108	4	US-09-025-769B-20	Sequence 20, Appl
40	38	49.4	108	4	US-08-450-363-12	Sequence 12, Appl
41	38	49.4	109	1	US-08-478-039-91	Sequence 91, Appl
42	38	49.4	109	1	US-08-476-349A-91	Sequence 91, Appl
43	38	49.4	109	3	US-09-202-181-2	Sequence 2, Appli
44	38	49.4	109	3	US-09-240-274-54	Sequence 54, Appl
45	38	49.4	109	3	US-09-240-274-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-154-750A-82
; Sequence 82, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-750A-82

Query Match 100.0%; Score 77; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db        110 PNHFRPAGLPEKY 122
```

RESULT 2
US-09-425-679E-11
; Sequence 11, Application US/09425679E
; Patent No. 6509444
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika L.
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679E
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 11
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Mustela vison
US-09-425-679E-11

  Query Match             92.2%;  Score 71;  DB 4;  Length 129;
  Best Local Similarity   84.6%;  Pred. No. 0.00018;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| :||| :||
Db        117 PNHFRPSGLPDKY 129


RESULT 3
US-09-425-679E-8
; Sequence 8, Application US/09425679E
; Patent No. 6509444
; GENERAL INFORMATION:
;  APPLICANT: McDonald, Thomas L.
;  APPLICANT:  Weber, Annika L.
;  TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
;  FILE REFERENCE: UNMC 63142
;  CURRENT APPLICATION NUMBER: US/09/425,679E
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: US 60/218,482
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/218,611
;  PRIOR FILING DATE: 2000-07-17
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Equus caballus
US-09-425-679E-8

  Query Match             88.3%;  Score 68;  DB 4;  Length 17;
  Best Local Similarity   84.6%;  Pred. No. 6.6e-05;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db          5 PNHFRPHGLPDKY 17


RESULT 4
'IS-09-029-345-1
  Sequence 1, Application US/09029345B
; Patent No. 6375949
; GENERAL INFORMATION:
;  APPLICANT: Hirano, et al.
;  TITLE OF INVENTION: Monoclonal Antibody Recognizing Serum Amyloid A
;  FILE REFERENCE: 112842-100
;  CURRENT APPLICATION NUMBER: US/09/029,345B
;  CURRENT FILING DATE: 1998-06-09
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-029-345-1

  Query Match             88.3%;  Score 68;  DB 4;  Length 104;
  Best Local Similarity   92.3%;  Pred. No. 0.00044;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||| |||||||||
Db         92 PNHDRPAGLPEKY 104


RESULT 5
US-09-425-679E-10
; Sequence 10, Application US/09425679E
; Patent No. 6509444
; GENERAL INFORMATION:
;  APPLICANT: McDonald, Thomas L.
;  APPLICANT:  Weber, Annika L.
;  TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
;  FILE REFERENCE: UNMC 63142
;  CURRENT APPLICATION NUMBER: US/09/425,679E
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: US 60/218,482
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/218,611
;  PRIOR FILING DATE: 2000-07-17
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Equus caballus
US-09-425-679E-10

  Query Match             88.3%;  Score 68;  DB 4;  Length 110;
  Best Local Similarity   84.6%;  Pred. No. 0.00047;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db         98 PNHFRPHGLPDKY 110


RESULT 6
US-09-240-274-64
; Sequence 64, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-4202
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain 002
US-09-240-274-64

  Query Match             58.4%;  Score 45;  DB 3;  Length 112;
  Best Local Similarity   50.0%;  Pred. No. 2.6;
  Matches    6;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 NHFRPAGLPEKY 13
              || ||:|:|:::
Db         52 NHNRPSGVPDRF 63


RESULT 7
US-09-252-991A-17856
; Sequence 17856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
```

```
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 17856
;   LENGTH: 845
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17856

  Query Match             54.5%;  Score 42;  DB 4;  Length 845;
  Best Local Similarity   80.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLP 10
              | | ||||||
Db        267 PLHRRPAGLP 276


RESULT 8
US-09-240-274-61
; Sequence 61, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-4202
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain N01
US-09-240-274-61

  Query Match             51.9%;  Score 40;  DB 3;  Length 109;
  Best Local Similarity   41.7%;  Pred. No. 16;
  Matches    5;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 NHFRPAGLPEKY 13
              |: ||:|:|:::
Db         51 NYRRPSGIPDRF 62


RESULT 9
US-09-252-991A-19920
; Sequence 19920, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 19920
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19920

  Query Match             51.9%;  Score 40;  DB 4;  Length 363;
  Best Local Similarity   41.7%;  Pred. No. 58;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEK 12
              |:| :| |:| :
Db        209 PHHLQPVGVPRR 220


RESULT 10
US-09-252-991A-23620
; Sequence 23620, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 23620
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23620

  Query Match             51.9%;  Score 40;  DB 4;  Length 497;
  Best Local Similarity   53.8%;  Pred. No. 80;
  Matches    7;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |   ||| || :|
Db        174 PGRGRPAALPRRY 186


RESULT 11
US-09-252-991A-29423
; Sequence 29423, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 29423
;   LENGTH: 762
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29423

  Query Match             51.9%;  Score 40;  DB 4;  Length 762;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    2;  Gaps    1;
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Qy          1 PNHF--RPAGLPEK 12
              |:||  |||| | :
Db        698 PHHFQGRPAGQPRR 711


RESULT 12
US-08-672-345C-3
; Sequence 3, Application US/08672345C
; Patent No. 5948658
;  GENERAL INFORMATION:
;    APPLICANT:  Landry Donald, W.
;    TITLE OF INVENTION:  ANTI-COCAINE CATALYTIC ANTIBODY
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper and Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/672,345C
;      FILING DATE:  24-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/51400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-672-345C-3

  Query Match             50.6%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity   41.7%;  Pred. No. 24;
  Matches    5;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NHFRPAGLPEKY 13
              |::|| |:| ::
Db         52 NNYRPPGVPARF 63


RESULT 13
US-08-672-345C-93
; Sequence 93, Application US/08672345C
; Patent No. 5948658
;  GENERAL INFORMATION:
;    APPLICANT:  Landry Donald, W.
;    TITLE OF INVENTION:  ANTI-COCAINE CATALYTIC ANTIBODY
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper and Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/672,345C
;      FILING DATE:  24-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/51400
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-672-345C-93

  Query Match             50.6%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity   41.7%;  Pred. No. 24;
  Matches    5;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NHFRPAGLPEKY 13
              |::|| |:| ::
Db         52 NNYRPPGVPARF 63


RESULT 14
US-09-214-095D-3
; Sequence 3, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
;  APPLICANT:  Landry, Donald
;  TITLE OF INVENTION:   ANTI-COCAINE CATALYTIC ANTIBODY
;  FILE REFERENCE:   51400-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/214,095D
;  CURRENT FILING DATE:  1999-07-19
;  NUMBER OF SEQ ID NOS:   121
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Murinae gen. Sp.
US-09-214-095D-3

  Query Match             50.6%;  Score 39;  DB 3;  Length 109;
  Best Local Similarity   41.7%;  Pred. No. 24;
  Matches    5;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NHFRPAGLPEKY 13
              |::|| |:| ::
Db         52 NNYRPPGVPARF 63


RESULT 15
US-09-214-095D-121
; Sequence 121, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
;  APPLICANT:  Landry, Donald
;  TITLE OF INVENTION:   ANTI-COCAINE CATALYTIC ANTIBODY
;  FILE REFERENCE:   51400-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/214,095D
;  CURRENT FILING DATE:  1999-07-19
;  NUMBER OF SEQ ID NOS:   121
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 121
;   LENGTH: 109
;   TYPE: PRT
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; ORGANISM: Murine
US-09-214-095D-121

Query Match 50.6%; Score 39; DB 3; Length 109;
Best Local Similarity 41.7%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 NHFRPAGLPEKY 13
              |::|| |:| ::
Db         52 NNYRPPGVPARF 63
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Search completed: August 18, 2003, 01:28:09
Job time : 43 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2003, 01:15:09 ; Search time 43 Seconds
(without alignments)
29.074 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	122	1	YLHUS	serum amyloid A1 p
2	77	100.0	122	1	YLHUA	serum amyloid A2 p
3	77	100.0	122	2	I39456	serum amyloid A2-b
4	77	100.0	122	4	JN0029	serum amyloid A3 p
5	74	96.1	116	2	D38645	amyloid A protein
6	74	96.1	116	2	E38645	amyloid A protein
7	74	96.1	119	1	YLDGA	amyloid protein AA
8	74	96.1	121	2	C38645	amyloid A protein
9	72	93.5	122	2	A35660	serum amyloid-rela
10	71	92.2	83	2	I71951	serum amyloid A -
11	71	92.2	129	2	B36451	serum amyloid A2 p
12	70	90.9	91	2	I71950	serum amyloid A -
13	70	90.9	122	2	A23521	serum amyloid A3 p
14	69	89.6	103	2	S06386	serum amyloid A pr
15	69	89.6	122	2	S32574	serum amyloid prot
16	69	89.6	122	2	JS0608	serum amyloid A pr
17	69	89.6	122	2	I46981	serum amyloid prot
18	69	89.6	122	2	I46982	serum amyloid prot
19	69	89.6	129	2	A36451	serum amyloid A1 p
20	68	88.3	110	2	A28573	serum amyloid A pr
21	68	88.3	130	2	A53167	serum amyloid A pr
22	67	87.0	122	2	A30248	serum amyloid AA-3
23	60	77.9	122	2	A23843	serum amyloid prot
24	60	77.9	122	2	I49496	amyloid A - mouse
25	58	75.3	122	2	B30248	serum amyloid AA1
26	58	75.3	122	2	C30248	serum amyloid AA2
27	57	74.0	122	2	B23843	serum amyloid prot
28	54	70.1	130	1	A38974	serum amyloid A4 p
29	46	59.7	404	2	T48098	hypothetical prote
30	46	59.7	1305	2	T23314	hypothetical prote
31	45	58.4	88	2	B41760	ovarian tumor prot
32	45	58.4	113	2	E44151	Ig lambda chain V
33	45	58.4	921	2	S42617	collagen alpha 1(I
34	45	58.4	1555	2	T18688	hypothetical prote
35	45	58.4	1973	2	G89608	protein B0272.5 [i
36	45	58.4	1973	2	T18686	hypothetical prote
37	44	57.1	106	2	A27227	amyloid protein A
38	44	57.1	297	2	AC0298	chelated iron tran
39	44	57.1	364	2	H82727	sugar ABC transpor
40	44	57.1	921	2	S40495	collagen alpha 1(I
41	42	54.5	123	2	S35302	B-cell protein 8HS
42	41	53.2	108	1	L5HUDL	Ig lambda chain V-
43	41	53.2	145	2	D81955	phosphotransferase
44	41	53.2	152	2	B81013	PTS system, IIAB c
45	41	53.2	413	2	T31051	transposase homolo

ALIGNMENTS

RESULT 1
YLHUS
serum amyloid A1 protein precursor [validated] - human
N;Alternate names: amyloid-related serum protein SAA
N;Contains: amyloid protein AA
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1982 #sequence_revision 08-Feb-1996 #text_change 08-Dec-2000
C;Accession: A22342; S09972; S09974; S09977; S09978; S12491; S12492; S20103; A60863; 3196
R;Sipe, J.D.; Colten, H.R.; Goldberger, G.; Edge, M.D.; Tack, B.F.; Cohen, A.S.; Whit
Biochemistry 24, 2931-2936, 1985
A;Title: Human serum amyloid A (SAA): biosynthesis and postsynthetic processing of pr
A;Reference number: A22342; MUID:85252712; PMID:3839415
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A22342
A;Molecule type: mRNA
A;Residues: 1-118,'S',120-122 <SIP>
A;Cross-references: GB:M10906; NID:g337747; PIDN:AAA60297.1; PID:g337748
R;Steinkasserer, A.; Weiss, E.H.; Schwaeble, W.; Linke, R.P.
Biochem. J. 268, 187-193, 1990
A;Title: Heterogeneity of human serum amyloid A protein: five different variants from
A;Reference number: S09972; MUID:90262544; PMID:1971508
A;Accession: S09972
A;Molecule type: mRNA
A;Residues: 8-72 <STE>
A;Cross-references: EMBL:X51443
A;Experimental source: clone pAS4
A;Note: allele SAA1*1 (SAA1-alpha)
A;Accession: S09974
A;Molecule type: mRNA
A;Residues: 73-122 <ST2>
A;Cross-references: EMBL:X51439; NID:g36311; PIDN:CAA35804.1; PID:g825714
A;Experimental source: clone pAS1
A;Note: allele SAA1*1 (SAA1-alpha)
A;Accession: S09977
A;Molecule type: mRNA
A;Residues: 73-74,'V',76-77,'N',79-122 <ST3>
A;Cross-references: EMBL:X51442; NID:g36314; PIDN:CAA35807.1; PID:g825717
A;Experimental source: clone pAS3-beta
A;Note: a variant of allele SAA1-beta
A;Accession: S09978
A;Molecule type: mRNA
A;Residues: 73-77,'N',79-122 <ST4>
A;Cross-references: EMBL:X51441
A;Experimental source: clone pAS3-alpha
R;Linke, R.P.
submitted to the EMBL Data Library, January 1990
A;Reference number: S12491
A;Accession: S12491
A;Molecule type: mRNA
A;Residues: 8-69,'LG' <LIN>
A;Cross-references: EMBL:X51443; NID:g36315; PIDN:CAA35808.1; PID:g939926

A;Experimental source: clone pAS4
A;Note: allele SAA1*1 (SAA1-alpha)
A;Accession: S12492
A;Molecule type: mRNA
A;Residues: 73-74,'V',76-77,'N',79-122 <LI2>
A;Cross-references: EMBL:X51441; NID:g36313; PIDN:CAA35806.1; PID:g825716
A;Experimental source: clone pAS3-alpha
R;Betts, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.
Scand. J. Immunol. 34, 471-482, 1991
A;Title: The human acute-phase serum amyloid A gene family: structure, evolution and exp
A;Reference number: S20103; MUID:92022342; PMID:1656519
A;Contents: allele SAA1*2b (SAA1-beta)
A;Accession: S20103
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-69,'A',71-74,'V',76-122 <BET>
A;Cross-references: EMBL:X56652; NID:g36307; PIDN:CAA39974.1; PID:g36308
R;Skinner, M.; Pinnette, A.; Travis, W.D.; Shwachman, H.; Cohen, A.S.
J. Lab. Clin. Med. 112, 413-417, 1988
A;Title: Isolation and sequence analysis of amyloid protein AA from a patient with cysti
A;Reference number: A60863; MUID:89010280; PMID:3171350
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A60863
A;Molecule type: protein
A;Residues: 19-94 <SKI>
R;Parmelee, D.C.; Titani, K.; Ericsson, L.H.; Eriksen, N.; Benditt, E.P.; Walsh, K.A.
Biochemistry 21, 3298-3303, 1982
A;Title: Amino acid sequence of amyloid-related apoprotein (apoSAA-1) from human high-de
A;Reference number: A90461; MUID:83000248; PMID:7115671
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A90461
A;Molecule type: protein
A;Residues: 19-122 <PAR>
A;Note: 70-Ala and 75-Val were also found
A;Note: this protein was isolated from the high-density lipoprotein fraction of serum
R;Sletten, K.; Marhaug, G.; Husby, G.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1039-1046, 1983
A;Title: The covalent structure of amyloid-related serum protein SAA from two patients w
A;Reference number: A91711; MUID:84030495; PMID:6629328
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A91711
A;Molecule type: protein
A;Residues: 19-40,'N',42-77,'N',79-92,'N',94-122 <SLE>
A;Note: at least three polymorphic forms of this protein have been found in a patient wi
leucine are found at position 76
R;Prelli, F.; Pras, M.; Frangione, B.
Biochemistry 26, 8251-8256, 1987
A;Title: Degradation and deposition of amyloid AA fibrils are tissue specific.
A;Reference number: A29419; MUID:88163487; PMID:3442653
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A29419
A;Molecule type: protein
A;Residues: 20-100 <PRE>
R;Westermark, G.T.; Sletten, K.; Westermark, P.
Scand. J. Immunol. 30, 605-613, 1989
A;Title: Massive vascular AA-amyloidosis: a histologically and biochemically distinctive
A;Reference number: A60431; MUID:90069444; PMID:2587936
A;Contents: allele SAA1*1 (SAA1-alpha)
A;Accession: A60431
A;Molecule type: protein
A;Residues: 19-98,'XXXX',103-105,'X',107 <WES>
R;Beach, C.M.; de Beer, M.C.; Sipe, J.D.; Loose, L.D.; de Beer, F.C.
Biochem. J. 282, 615-620, 1992
A;Title: Human serum amyloid A protein. Complete amino acid sequence of a new variant.
A;Reference number: S21260; MUID:92189607; PMID:1546977
A;Contents: allele SAA1*2a (SAA1-beta)
A;Accession: S21261
A;Molecule type: protein
A;Residues: 19-69,'A',71-74,'V',76-89,'D',91-122 <BEA>
A;Accession: S21260
A;Molecule type: protein
A;Residues: 20-69,'A',71-74,'V',76-89,'D',91-122 <BE2>
R;Baba, S.; Takahashi, T.; Kasama, T.; Fujie, M.; Shirasawa, H.
Arch. Biochem. Biophys. 303, 361-366, 1993
A;Title: A novel polymorphism of human serum amyloid A protein, SAAlgamma, is charact
A;Reference number: S33864; MUID:93290347; PMID:8512321
A;Contents: allele SAA1-gamma
A;Accession: S33864
A;Molecule type: protein
A;Residues: 19-69,'A',71-122 <BAB>
R;Baba, S.; Takahashi, T.; Kasama, T.; Shirasawa, H.
Biochim. Biophys. Acta 1180, 195-200, 1992
A;Title: Identification of two novel amyloid A protein subsets coexisting in an indiv
A;Reference number: A56867; MUID:93099171; PMID:1463770
A;Contents: allele SAA1-gamma (allele 52,57-Ala)
A;Accession: A56867
A;Molecule type: protein
A;Residues: 65-69,'A',71-80 <BA2>
A;Experimental source: amyloid fibrils, thyroid gland of rheumatoid arthritis patient
A;Note: sequence extracted from NCBI backbone (NCBIP:121042)
R;Moyner, K.; Sletten, K.; Husby, G.; Natvig, J.B.
Scand. J. Immunol. 11, 549-554, 1980
A;Title: An unusually large (83 amino acid residues) amyloid fibril protein AA from a
A;Reference number: A94234; MUID:80213686; PMID:6155694
A;Contents: Bol
A;Accession: A94234
A;Molecule type: protein
A;Residues: 19-40,'N',42-83,'E',85-92,'N',94-95,'SEATVK' <MOY>
A;Note: 70-Ala and 71-Arg were also found
A;Note: this protein is from a patient with Waldenstrom's macroglobulinemia
R;Sletten, K.; Husby, G.
Eur. J. Biochem. 41, 117-125, 1974
A;Title: The complete amino-acid sequence of non-immunoglobulin amyloid fibril protei
A;Reference number: A91215; MUID:74120351; PMID:4816450
A;Contents: Th
A;Accession: A91215
A;Molecule type: protein
A;Residues: 19-40,'N',42-92,'N',94 <SL3>
A;Note: this protein is from a patient with juvenile rheumatoid arthritis
R;Sletten, K.; Husby, G.; Natvig, J.B.
Biochem. Biophys. Res. Commun. 69, 19-25, 1976
A;Title: The complete amino acid sequence of an amyloid fibril protein AA of unusual
A;Reference number: A90195; MUID:76160745; PMID:1259755
A;Contents: Jl
A;Accession: A90195
A;Molecule type: protein
A;Residues: 19-40,'N',42-77,'N',79-82 <SL2>
A;Note: 19-Arg is missing from some of the molecules
A;Note: this protein is from a patient with ankylosing spondylitis
R;Gorevic, P.D.; Prelli, F.C.; Wright, J.; Pras, M.; Frangione, B.
J. Clin. Invest. 83, 836-843, 1989
A;Title: Systemic senile amyloidosis. Identification of a new prealbumin (transthyret
opathy.
A;Reference number: A30323; MUID:89155805; PMID:2646319
A;Accession: B30323
A;Molecule type: protein
A;Residues: 19-29 <GOR>
R;Uhlar, C.M.; Burgess, C.J.; Sharp, P.M.; Whitehead, A.S.
Genomics 19, 228-235, 1994
A;Title: Evolution of the serum amyloid A (SAA) protein superfamily.
A;Reference number: A38975; MUID:94245191; PMID:8188253
A;Contents: annotation
R;Kluve-Beckerman, B.; Dwulet, F.E.; Benson, M.D.
J. Clin. Invest. 82, 1670-1675, 1988
A;Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in
A;Reference number: I39454; MUID:89034862; PMID:3183061
A;Accession: I39454
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-122 <RES>
A;Cross-references: GB:M23698; NID:g758678; PIDN:AAA64799.1; PID:g758679
C;Genetics:
A;Gene: GDB:SAA1; SAA
A;Cross-references: GDB:120364; OMIM:104750
A;Map position: 11p15.1-11p15.1
A;Introns: 31/1; 77/2

C;Superfamily: amyloid protein
C;Keywords: acute phase; amyloid; HDL; polymorphism
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-122/Product: (or 20-122) serum amyloid A1 protein #status experimental <APA>
F;19-94/Product: (or 20-94) amyloid protein AA #status experimental <AP3>

Query Match 100.0%; Score 77; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||||
Db 110 PNHFRPAGLPEKY 122

RESULT 2
YLHUA
serum amyloid A2 protein precursor [validated] - human
N;Alternate names: amyloid IV; amyloid protein AA (FMF); amyloid-related serum protein S
;Species: Homo sapiens (man)
;Date: 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change 08-Dec-2000
C;Accession: A27902; S20104; S09975; S09976; S09973; B38974; A28445; A92763; A92112; A91
R;Kluve-Beckerman, B.; Long, G.L.; Benson, M.D.
Biochem. Genet. 24, 795-803, 1986
A;Title: DNA sequence evidence for polymorphic forms of human serum amyloid A (SAA).
A;Reference number: A27902; MUID:87099785; PMID:3800865
A;Contents: allele SAA2*1 (SAA2-alpha)
A;Accession: A27902
A;Molecule type: mRNA
A;Residues: 1-122 <KLU>
A;Cross-references: GB:M26152; NID:g1160968; PIDN:AAA85338.1; PID:g1160969
R;Betts, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.
Scand. J. Immunol. 34, 471-482, 1991
A;Title: The human acute-phase serum amyloid A gene family: structure, evolution and exp
A;Reference number: S20103; MUID:92022342; PMID:1656519
A;Contents: allele SAA2*1 (SAA2-alpha)
A;Accession: S20104
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 32-122 <BET>
A;Cross-references: EMBL:X56653; NID:g36309; PIDN:CAA39975.1; PID:g36310
R;Steinkasserer, A.; Weiss, E.H.; Schwaeble, W.; Linke, R.P.
Biochem. J. 268, 187-193, 1990
A;Title: Heterogeneity of human serum amyloid A protein: five different variants from or
A;Reference number: S09972; MUID:90262544; PMID:1971508
A;Accession: S09975
A;Molecule type: mRNA
A;Residues: 1-55 <STE>
;Cross-references: EMBL:X51444; NID:g36316; PIDN:CAA35809.1; PID:g36317
A;Experimental source: clone pAS6
A;Note: allele SAA2*1 (SAA2-alpha)
A;Accession: S09976
A;Molecule type: mRNA
A;Residues: 4-122 <ST2>
A;Cross-references: EMBL:X51445; NID:g36320; PIDN:CAA35810.1; PID:g36321
A;Experimental source: clone pAS8
A;Note: allele SAA2*1 (SAA2-alpha)
A;Accession: S09973
A;Molecule type: mRNA
A;Residues: 73-88,'R',90-122 <ST3>
A;Cross-references: EMBL:X51440; NID:g36312; PIDN:CAA35805.1; PID:g825715
A;Experimental source: clone pAS2
A;Note: allele SAA2*2 (SAA2-beta)
R;Steel, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.
Genomics 16, 447-454, 1993
A;Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely linke
A;Reference number: A38974; MUID:93300520; PMID:7686132
A;Contents: allele SAA2*2 (SAA2-beta)
A;Accession: B38974
A;Molecule type: DNA
A;Residues: 1-88,'R',90-122 <ST4>
A;Cross-references: GB:L05921
R;Woo, P.; Sipe, J.; Dinarello, C.A.; Colten, H.R.
J. Biol. Chem. 262, 15790-15795, 1987
A;Title: Structure of a human serum amyloid A gene and modulation of its expression
A;Reference number: A28445; MUID:88058926; PMID:2890635
A;Contents: allele SAA2*2 (SAA2-beta)
A;Accession: A28445
A;Molecule type: DNA
A;Residues: 1-14,'G',16-88,'R',90-122 <WOO>
A;Cross-references: GB:J03474; NID:g337742; PIDN:AAB59539.1; PID:g337743
R;Levin, M.; Franklin, E.C.; Frangione, B.; Pras, M.
J. Clin. Invest. 51, 2773-2776, 1972
A;Title: The amino acid sequence of a major nonimmunoglobulin component of some amyl
A;Reference number: A92763; MUID:72268653; PMID:5056669
A;Contents: allele SAA2*2 (SAA2-beta)
A;Accession: A92763
A;Molecule type: protein
A;Residues: 19-70,'R',72-88,'R',90-94 <LEV>
A;Note: this protein is from a patient with familial Mediterranean fever
A;Note: the sequence of residues 19-72 of amyloid protein AA from a patient with tub
R;Ein, D.; Kimura, S.; Terry, W.D.; Magnotta, J.; Glenner, G.G.
J. Biol. Chem. 247, 5653-5655, 1972
A;Title: Amino acid sequence of an amyloid fibril protein of unknown origin.
A;Reference number: A92112; MUID:72266694; PMID:5055786
A;Accession: A92112
A;Molecule type: protein
A;Residues: 19-63 <EIN>
A;Note: this amyloid IV was isolated from a patient with rheumatoid arthritis
R;Benditt, E.P.; Eriksen, N.; Hermodson, M.A.; Ericsson, L.H.
FEBS Lett. 19, 169-173, 1971
A;Title: The major proteins of human and monkey amyloid substance: common properties
A;Reference number: A91345
A;Accession: A91345
A;Molecule type: protein
A;Residues: 19-42 <BEN>
A;Note: the amino-terminal tripeptide is sometimes missing
A;Note: this protein is from a patient with generalized amyloidosis associated with
R;Baba, S.; Takahashi, T.; Kasama, T.; Shirasawa, H.
Biochim. Biophys. Acta 1180, 195-200, 1992
A;Title: Identification of two novel amyloid A protein subsets coexisting in an indi
A;Reference number: A56867; MUID:93099171; PMID:1463770
A;Contents: allele SAA2*1 (SAA2-alpha)
A;Accession: B56867
A;Molecule type: protein
A;Residues: 65-80 <BAB>
A;Experimental source: amyloid fibrils, thyroid gland of rhematoid arthritis patient
A;Note: sequence extracted from NCBI backbone (NCBIP:121046)
R;Kluve-Beckerman, B.; Dwulet, F.E.; Benson, M.D.
J. Clin. Invest. 82, 1670-1675, 1988
A;Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins i
A;Reference number: I39454; MUID:89034862; PMID:3183061
A;Accession: I39455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-122 <RES>
A;Cross-references: GB:M23699; NID:g758680; PIDN:AAA64800.1; PID:g758681
C;Genetics:
A;Gene: GDB:SAA2
A;Cross-references: GDB:132592; OMIM:104751
A;Map position: 11p15.1-11p15.1
A;Introns: 31/1; 77/2
C;Superfamily: amyloid protein
C;Keywords: acute phase; amyloid; polymorphism
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-94/Product: serum amyloid A2 protein #status experimental <MAT>

Query Match 100.0%; Score 77; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13
||||||||||||||
Db 110 PNHFRPAGLPEKY 122

```
RESULT 3
I39456
serum amyloid A2-beta - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999
C;Accession: I39456
R;Kluve-Beckerman, B.; Dwulet, F.E.; Benson, M.D.
J. Clin. Invest. 82, 1670-1675, 1988
A;Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in on
A;Reference number: I39454; MUID:89034862; PMID:3183061
A;Accession: I39456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-122 <RES>
A;Cross-references: GB:M23700; NID:g758682; PIDN:AAA64801.1; PID:g758683
C;Genetics:
A;Gene: GDB:SAA2
A;Cross-references: GDB:132592; OMIM:104751
A;Map position: 11p15.1-11p15.1
C;Superfamily: amyloid protein

  Query Match             100.0%;  Score 77;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 6e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db        110 PNHFRPAGLPEKY 122


RESULT 4
JN0029
serum amyloid A3 pseudogene - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 17-May-1996 #text_change 20-Apr-2000
C;Accession: JN0029
R;Sack Jr., G.H.; Talbot Jr., C.C.
Gene 84, 509-515, 1989
A;Title: The human serum amyloid A (SAA)-encoding gene GSAA1: nucleotide sequence and pc
A;Reference number: JN0029
A;Accession: JN0029
A;Status: conceptual translation of pseudogene
A;Molecule type: DNA
A;Residues: 1-122 <SAC>
A;Cross-references: EMBL:X13895; NID:g36305; PIDN:CAA32096.1; PID:g36306
R;Steel, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.
Genomics 16, 447-454, 1993
A;Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely linke
  Reference number: A38974; MUID:93300520; PMID:7686132
  Contents: annotation
A;Note: references cited confirm a frameshift error between codons 30 and 32 that leads
C;Genetics:
A;Gene: GDB:SAA3; GSAA1
A;Cross-references: GDB:132593
A;Map position: 11p15.1-p14
A;Introns: 31/1; 77/2
C;Keywords: pseudogene

  Query Match             100.0%;  Score 77;  DB 4;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 6e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db        110 PNHFRPAGLPEKY 122


RESULT 5
D38645
amyloid A protein DSAA85 precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
C;Accession: D38645
R;Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A;Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A;Reference number: A38645; MUID:91139635; PMID:1995613
A;Accession: D38645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <SEL>
A;Cross-references: GB:M59174; NID:g164065; PIDN:AAA62765.1; PID:g164066
C;Superfamily: amyloid protein

  Query Match             96.1%;  Score 74;  DB 2;  Length 116;
  Best Local Similarity   92.3%;  Pred. No. 1.9e-05;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||:||
Db        104 PNHFRPAGLPDKY 116


RESULT 6
E38645
amyloid A protein DSAA86 precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
C;Accession: E38645
R;Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A;Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A;Reference number: A38645; MUID:91139635; PMID:1995613
A;Accession: E38645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <SEL>
A;Cross-references: GB:M59175; NID:g164067; PIDN:AAA51457.1; PID:g164068
C;Superfamily: amyloid protein

  Query Match             96.1%;  Score 74;  DB 2;  Length 116;
  Best Local Similarity   92.3%;  Pred. No. 1.9e-05;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||:||
Db        104 PNHFRPAGLPDKY 116


RESULT 7
YLDGA
amyloid protein AA precursor (clone DSAA15) - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 11-May-2000
C;Accession: A38645; JL0110
R;Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A;Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A;Reference number: A38645; MUID:91139635; PMID:1995613
A;Accession: A38645
A;Molecule type: mRNA
A;Residues: 1-119 <SEL>
A;Cross-references: GB:M59171; NID:g164059; PIDN:AAA62762.1; PID:g164060
R;Kluve-Beckerman, B.; Dwulet, F.E.; DiBartola, S.P.; Benson, M.D.
Comp. Biochem. Physiol. B 94, 175-183, 1989
A;Title: Primary structures of dog and cat amyloid A proteins: comparison to human AA
A;Reference number: JL0110; MUID:90091422; PMID:2598632
A;Accession: JL0110
A;Molecule type: protein
A;Residues: 9-101 <KLU>
A;Note: 25-Trp was also found
C;Comment: This protein is the main constituent of reactive amyloid fibrils in man an
.
C;Comment: The extracellular deposits formed by this protein are highly insoluble and
C;Superfamily: amyloid protein
C;Keywords: amyloid; pyroglutamic acid
```

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F;1-8/Domain: signal sequence (fragment) #status predicted <SIG>
F;9-101/Product: amyloid protein AA #status experimental <MAT>
F;9/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

  Query Match             96.1%;  Score 74;  DB 1;  Length 119;
  Best Local Similarity   92.3%;  Pred. No. 1.9e-05;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||||||:||
Db        107 PNHFRPAGLPDKY 119


RESULT 8
C38645
amyloid A protein DSAA32 precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
C;Accession: C38645
R;Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.
  Biol. Chem. 266, 3505-3510, 1991
A;Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by cDN
A;Reference number: A38645; MUID:91139635; PMID:1995613
A;Accession: C38645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SEL>
A;Cross-references: GB:M59173; NID:g164063; PIDN:AAA62764.1; PID:g164064
C;Superfamily: amyloid protein

  Query Match             96.1%;  Score 74;  DB 2;  Length 121;
  Best Local Similarity   92.3%;  Pred. No. 1.9e-05;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||||||:||
Db        109 PNHFRPAGLPDKY 121


RESULT 9
A35660
serum amyloid-related protein SAA3 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 20-Aug-1999
C;Accession: A35660
R;Gervais, C.; Suh, M.
Mol. Cell. Biol. 10, 4412-4414, 1990
A;Title: Serum amyloid A protein-related mRNA expression in herpes simplex virus type 2-
  Reference number: A35660; MUID:90318412; PMID:2164641
A;Accession: A35660
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <GER>
A;Cross-references: GB:M33431; NID:g191440; PIDN:AAA37098.1; PID:g305362
C;Superfamily: amyloid protein

  Query Match             93.5%;  Score 72;  DB 2;  Length 122;
  Best Local Similarity   92.3%;  Pred. No. 4.3e-05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||| ||
Db        110 PNHFRPAGLPSKY 122


RESULT 10
I71951
serum amyloid A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I71951
R;Yamamoto, K.
J. Immunol. 139, 1683-1688, 1987
A;Title: Structural diversity of murine serum amyloid A genes: Evolutionary implicat
A;Reference number: I55984; MUID:87309776; PMID:3624868
A;Accession: I71951
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-83 <RES>
A;Cross-references: GB:M17790; NID:g200920; PIDN:AAA40089.1; PID:g200921
C;Genetics:
A;Introns: 38/2
C;Superfamily: amyloid protein

  Query Match             92.2%;  Score 71;  DB 2;  Length 83;
  Best Local Similarity   84.6%;  Pred. No. 4.4e-05;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||:|||||||:||
Db         71 PNHYRPAGLPDKY 83


RESULT 11
B36451
serum amyloid A2 precursor - American mink
C;Species: Mustela vison (American mink)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 20-Aug-1999
C;Accession: B36451
R;Marhaug, G.; Husby, G.; Dowton, S.B.
J. Biol. Chem. 265, 10049-10054, 1990
A;Title: Mink serum amyloid A protein. Expression and primary structure based on cDN
A;Reference number: A36451; MUID:90277614; PMID:2351648
A;Accession: B36451
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <MAR>
A;Cross-references: GB:M34954; GB:J05445; NID:g164267; PIDN:AAA30969.1; PID:g164268
C;Superfamily: amyloid protein

  Query Match             92.2%;  Score 71;  DB 2;  Length 129;
  Best Local Similarity   84.6%;  Pred. No. 6.8e-05;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||:|||:||
Db        117 PNHFRPSGLPDKY 129


RESULT 12
I71950
serum amyloid A - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I71950
R;Yamamoto, K.
J. Immunol. 139, 1683-1688, 1987
A;Title: Structural diversity of murine serum amyloid A genes: Evolutionary implicat.
A;Reference number: I55984; MUID:87309776; PMID:3624868
A;Accession: I71950
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-91 <RES>
A;Cross-references: GB:M17792; NID:g200917; PIDN:AAA40088.1; PID:g200919
C;Genetics:
A;Introns: 46/2
C;Superfamily: amyloid protein

  Query Match             90.9%;  Score 70;  DB 2;  Length 91;
  Best Local Similarity   84.6%;  Pred. No. 7.1e-05;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||||||::|
Db         79 PNHFRPAGLPKRY 91
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```
RESULT 13
A23521
serum amyloid A3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Aug-1999
C;Accession: A23521; B23521; C23843; I49495
R;Stearman, R.S.; Lowell, C.A.; Peltzman, C.G.; Morrow, J.F.
Nucleic Acids Res. 14, 797-809, 1986
A;Title: The sequence and structure of a new serum amyloid A gene.
A;Reference number: A23521; MUID:86120372; PMID:3003697
A;Accession: A23521
A;Molecule type: DNA
A;Residues: 1-30 <ST1>
A;Accession: B23521
A;Molecule type: mRNA
A;Residues: 27-122 <ST2>
A;Cross-references: GB:X03479; NID:g54035; PIDN:CAA27199.1; PID:g817998
R;Lowell, C.A.; Potter, D.A.; Stearman, R.S.; Morrow, J.F.
J. Biol. Chem. 261, 8442-8452, 1986
  Title: Structure of the murine serum amyloid A gene family. Gene conversion.
A;Reference number: A23843; MUID:86250747; PMID:3013853
A;Accession: C23843
A;Molecule type: DNA
A;Residues: 1-122 <LOW>
R;Stearman, R.S.; Lowell, C.A.; Pearson, W.R.; Morrow, J.F.
Ann. N. Y. Acad. Sci. 389, 106-115, 1982
A;Title: Regulation of synthesis of amyloid A-related protein.
A;Reference number: I49495; MUID:82229376; PMID:6953913
A;Accession: I49495
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 27-64 <RES>
A;Cross-references: GB:M25467; NID:g191929; PIDN:AAA37231.1; PID:g191930
C;Genetics:
A;Introns: 31/1; 77/2
C;Superfamily: amyloid protein
C;Keywords: acute phase; amyloid
F;19-122/Product: serum amyloid-related protein SAA3 #status predicted <MAT>

  Query Match             90.9%;  Score 70;  DB 2;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 9.5e-05;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||::|
Db        110 PNHFRPAGLPKRY 122


  SULT 14
S06386
serum amyloid A protein precursor - American mink
C;Species: Mustela vison (American mink)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 05-Aug-1994
C;Accession: S06386
R;Syversen, V.; Sletten, K.; Marhaug, G.; Husby, G.; Lium, B.
Scand. J. Immunol. 26, 763-767, 1987
A;Title: The amino acid sequence of serum amyloid A (SAA) protein in mink.
A;Reference number: S06386; MUID:88099357; PMID:3423742
A;Accession: S06386
A;Molecule type: protein
A;Residues: 1-103 <SYV>
A;Note: 10-Val, 67-Val, and 71-Phe were also found
C;Superfamily: amyloid protein
C;Keywords: amyloid; pyroglutamic acid
F;1-103/Product: amyloid protein A, serum #status experimental <MAT1>
F;1-64/Product: amyloid protein A, amyloid (long form) #status experimental <MAT2>
F;1-53/Product: amyloid protein A, amyloid (short form) #status experimental <MAT3>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

  Query Match             89.6%;  Score 69;  DB 2;  Length 103;
  Best Local Similarity   84.6%;  Pred. No. 0.00012;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db         91 PNHFRPPGLPDKY 103


RESULT 15
S32574
serum amyloid protein SAA - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S32574
R;Mitchell, T.I.; Coon, C.I.; Brinckerhoff, C.E.
J. Clin. Invest. 87, 1177-1185, 1991
A;Title: Serum amyloid A (SAA3) produced by rabbit synovial fibroblasts treated with
A;Reference number: S32574; MUID:91185595; PMID:1849144
A;Accession: S32574
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <MIT>
A;Cross-references: EMBL:M64696; NID:g165698; PIDN:AAA31464.1; PID:g165699
C;Superfamily: amyloid protein

  Query Match             89.6%;  Score 69;  DB 2;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 0.00014;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db        110 PNHFRPKGLPDKY 122


Search completed: August 18, 2003, 01:27:14
Job time : 45 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2003, 23:55:27 ; Search time 37 Seconds
(without alignments)
16.523 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	122	1	SAA3_HUMAN	P22614 homo sapien
2	77	100.0	122	1	SAA_HUMAN	P02735 homo sapien
3	74	96.1	112	1	SAA_BOVIN	P35541 bos taurus
4	74	96.1	129	1	SAA_CANFA	P19708 canis famil
5	72	93.5	122	1	SAA3_MESAU	P19453 mesocricetu
6	71	92.2	102	1	SAA5_MESAU	P81491 mesocricetu
7	71	92.2	129	1	SAA2_MUSVI	P02739 mustela vis
8	70	90.9	122	1	SAA3_MOUSE	P04918 mus musculu
9	69	89.6	112	1	SAA_SHEEP	P42819 ovis aries
10	69	89.6	122	1	SAA1_RABIT	P53614 oryctolagus
11	69	89.6	122	1	SAA2_RABIT	P22000 oryctolagus
12	69	89.6	122	1	SAA3_RABIT	P35543 oryctolagus
13	69	89.6	129	1	SAA1_MUSVI	P18575 mustela vis
14	68	88.3	110	1	SAA_HORSE	P19857 equus cabal
15	68	88.3	130	1	SAA4_MOUSE	P31532 mus musculu
16	60	77.9	122	1	SAA1_MOUSE	P05366 mus musculu
17	58	75.3	122	1	SAA1_MESAU	P20726 mesocricetu
18	58	75.3	122	1	SAA2_MESAU	P20727 mesocricetu
19	57	74.0	122	1	SAA2_MOUSE	P05367 mus musculu
20	56	72.7	127	1	SAA_ANAPL	P02740 anas platyr
21	54	70.1	130	1	SAA4_HUMAN	P35542 homo sapien
22	47	61.0	127	1	SAA_MACEU	P53613 macropus eu
23	44	57.1	297	1	YFED_YERPE	Q56955 yersinia pe
24	44	57.1	921	1	CA19_MOUSE	Q05722 mus musculu
25	41	53.2	108	1	LV5A_HUMAN	P01719 homo sapien
26	41	53.2	646	1	YEGI_ECO57	Q8x7j8 escherichia
27	41	53.2	648	1	YEGI_ECOLI	P76393 escherichia
28	41	53.2	864	1	SBE2_YEAST	P42223 saccharomyc
29	40	51.9	412	1	KAPR_EMENI	O59922 emericella
30	40	51.9	676	1	KALM_CHICK	P33005 gallus gall
31	39	50.6	109	1	LV1I_HUMAN	P06888 homo sapien
32	39	50.6	111	1	LV1D_HUMAN	P01702 homo sapien
33	39	50.6	123	1	VPR3_HUMAN	Q9uki3 homo sapien
34	39	50.6	130	1	LV1G_HUMAN	P06316 homo sapien
35	39	50.6	154	1	ELYS_HALRU	P04552 haliotis ru
36	39	50.6	446	1	CLUS_PIG	Q29549 sus scrofa
37	39	50.6	448	1	CLUS_MOUSE	Q06890 mus musculu
38	39	50.6	520	1	JRKY_HUMAN	O75564 homo sapien
39	39	50.6	557	1	JRKY_MOUSE	Q60976 mus musculu
40	39	50.6	680	1	KALM_HUMAN	P23352 homo sapien
41	39	50.6	809	1	DCML_OLICA	P19919 oligotropha
42	39	50.6	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
43	38	49.4	106	1	LV4A_HUMAN	P01715 homo sapien
44	38	49.4	111	1	LV3B_HUMAN	P80748 homo sapien
45	38	49.4	289	1	E1A_ADE02	P03254 human adeno

ALIGNMENTS

RESULT 1
SAA3_HUMAN
ID SAA3_HUMAN STANDARD; PRT; 122 AA.
AC P22614; O95735;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative serum amyloid A-3 protein.
GN SAA3P OR SAA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128298; PubMed=2558975;
RA Sack G.H. Jr., Talbot C.C. Jr.;
RT "The human serum amyloid A (SAA)-encoding gene GSAA1: nucleotide
RT sequence and possible autocrine-collagenase-inducer function.";
RL Gene 84:509-515(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92096115; PubMed=1755958;
RA Kluve-Beckerman B., Drumm M.L., Benson M.D.;
RT "Nonexpression of the human serum amyloid A three (SAA3) gene.";
RL DNA Cell Biol. 10:651-661(1991).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -!- CAUTION: This is probably the product of a pseudogene.
CC ---

CC ---
DR EMBL; X13895; CAA32096.1; ALT_INIT.
DR EMBL; S73444; -; NOT_ANNOTATED_CDS.
DR PIR; JN0029; JN0029.
DR Genew; HGNC:10515; SAA3P.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Hypothetical protein.
FT CONFLICT 5 5 T -> Y (IN REF. 2).
FT CONFLICT 32 32 A -> T (IN REF. 2).
FT CONFLICT 37 37 R -> K (IN REF. 2).
FT CONFLICT 49 49 K -> N (IN REF. 2).
FT CONFLICT 57 57 R -> W (IN REF. 2).
FT CONFLICT 67 69 PGG -> LGA (IN REF. 2).
SQ SEQUENCE 122 AA; 13440 MW; 70F0BCC052E08472 CRC64;

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  Query Match           100.0%;  Score 77;  DB 1;  Length 122;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db        110 PNHFRPAGLPEKY 122


RESULT 2
SAA_HUMAN
ID   SAA_HUMAN      STANDARD;      PRT;   122 AA.
AC   P02735; P02736; P02737; Q16730; Q16835; Q16879; Q96QN0;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Serum amyloid A protein precursor (SAA) [Contains: Amyloid protein A
DE   (Amyloid fibril protein AA)].
GN   SAA1 AND SAA2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85252712; PubMed=3839415;
RA   Sipe J.D., Colten H.R., Goldberger G., Edge M.D., Tack B.F.,
RA   Cohen A.S., Whitehead A.S.;
RT   "Human serum amyloid A (SAA): biosynthesis and postsynthetic
RT   processing of preSAA and structural variants defined by complementary
RT   DNA.";
RL   Biochemistry 24:2931-2936(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88058926; PubMed=2890635;
RA   Woo P., Sipe J., Dinarello C.A., Colten H.R.;
RT   "Structure of a human serum amyloid A gene and modulation of its
RT   expression in transfected L cells.";
RL   J. Biol. Chem. 262:15790-15795(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87099785; PubMed=3800865;
RA   Kluve-Beckerman B., Long G.L., Benson M.D.;
RT   "DNA sequence evidence for polymorphic forms of human serum amyloid A
RT   (SAA).";
RL   Biochem. Genet. 24:795-803(1986).
RN   [4]
RP   SEQUENCE FROM N.A. (SAA1 AND SAA2).
RC   TISSUE=Liver;
RX   MEDLINE=89034862; PubMed=3183061;
RA   Kluve-Beckerman B., Dwulet F.E., Benson M.D.;
RT   "Human serum amyloid A. Three hepatic mRNAs and the corresponding
RT   proteins in one person.";
RL   J. Clin. Invest. 82:1670-1675(1988).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=90262544; PubMed=1971508;
RA   Steinkasserer A., Weiss E.H., Schwaeble W., Linke R.P.;
RT   "Heterogeneity of human serum amyloid A protein. Five different
RT   variants from one individual demonstrated by cDNA sequence
RT   analysis.";
RL   Biochem. J. 268:187-193(1990).
RN   [6]
RP   SEQUENCE FROM N.A. (SAA1 AND SAA2 ALPHA).
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 19-122.
RX   MEDLINE=83000248; PubMed=7115671;
RA   Parmelee D.C., Titani K., Ericsson L.H., Eriksen N., Benditt E.P.,
RA   Walsh K.A.;
RT   "Amino acid sequence of amyloid-related apoprotein (apoSAA1) from
RT   human high-density lipoprotein.";
RL   Biochemistry 21:3298-3303(1982).
RN   [8]
RP   SEQUENCE OF 19-122 (VARIANT 1-BETA).
RX   MEDLINE=92189607; PubMed=1546977;
RA   Beach C.M., de Beer M.C., Sipe J.D., Loose L.D., de Beer F.C.;
RT   "Human serum amyloid A protein. Complete amino acid sequence of a new
RT   variant.";
RL   Biochem. J. 282:615-620(1992).
RN   [9]
RP   SEQUENCE OF 20-100.
RX   MEDLINE=88163487; PubMed=3442653;
RA   Prelli F., Pras M., Frangione B.;
RT   "Degradation and deposition of amyloid AA fibrils are tissue
RT   specific.";
RL   Biochemistry 26:8251-8256(1987).
RN   [10]
RP   SEQUENCE OF 19-94 (FAMILIAL MEDITERRANEAN FEVER PATIENT).
RX   MEDLINE=72268653; PubMed=5056669;
RA   Levin M., Franklin E.C., Frangione B., Pras M.;
RT   "The amino acid sequence of a major nonimmunoglobulin component of
RT   some amyloid fibrils.";
RL   J. Clin. Invest. 51:2773-2776(1972).
RN   [11]
RP   SEQUENCE OF 19-94 (TUBERCULOSIS PATIENT).
RX   MEDLINE=72266694; PubMed=5055786;
RA   Ein D., Kimura S., Terry W.D., Magnotta J., Glenner G.G.;
RT   "Amino acid sequence of an amyloid fibril protein of unknown origin.";
RL   J. Biol. Chem. 247:5653-5655(1972).
RN   [12]
RP   SEQUENCE OF 19-94 (TH).
RX   MEDLINE=74120351; PubMed=4816450;
RA   Sletten K., Husby G.;
RT   "The complete amino-acid sequence of non-immunoglobulin amyloid
RT   fibril protein AS in rheumatoid arthritis.";
RL   Eur. J. Biochem. 41:117-125(1974).
RN   [13]
RP   SEQUENCE OF 19-82 (JL).
RX   MEDLINE=76160745; PubMed=1259755;
RA   Sletten K., Husby G., Natvig J.B.;
RT   "The complete amino acid sequence of an amyloid fibril protein AA1 of
RT   unusual size (64 residues).";
RL   Biochem. Biophys. Res. Commun. 69:19-25(1976).
RN   [14]
RP   SEQUENCE OF 19-101 (BOL).
RX   MEDLINE=80213686; PubMed=6155694;
RA   Moyner K., Sletten K., Husby G., Natvig J.B.;
RT   "An unusually large (83 amino acid residues) amyloid fibril protein
RT   AA from a patient with Waldenstrom's macroglobulinaemia and
RT   amyloidosis.";
RL   Scand. J. Immunol. 11:549-554(1980).
RN   [15]
RP   SEQUENCE OF 19-42.
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RA   Benditt E.P., Eriksen N., Hermodson M.A., Ericsson L.H.;
RT   "The major proteins of human and monkey amyloid substance: common
RT   properties including unusual N-terminal amino acid sequences.";
RL   FEBS Lett. 19:169-173(1971).
RN   [16]
RP   SEQUENCE OF 32-122 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=92022342; PubMed=1656519;
RA   Betts J., Edbrooke M., Thakker R., Woo P.;
RT   "The human acute-phase serum amyloid A gene family: structure,
RT   evolution and expression in hepatoma cells.";
RL   Scand. J. Immunol. 34:471-482(1991).
RN   [17]
RP   VARIANT 1-GAMMA.
RX   MEDLINE=93290347; PubMed=8512321;
RA   Baba S., Takahashi T., Kasama T., Fujie M., Shirasawa H.;
RT   "A novel polymorphism of human serum amyloid A protein, SAA1 gamma,
RT   is characterized by alanines at both residues 52 and 57.";
RL   Arch. Biochem. Biophys. 303:361-366(1993).
RN   [18]
RP   PARTIAL SEQUENCE (VARIOUS FORMS), AND METHYLATION OF ASN-101.
RX   MEDLINE=96377164; PubMed=8783012;
RA   Ducret A., Bruun C.F., Bures E.J., Marhaug G., Husby G.,
RA   Aebersold R.;
RT   "Characterization of human serum amyloid A protein isoforms separated
RT   by two-dimensional electrophoresis by liquid
RT   chromatography/electrospray ionization tandem mass spectrometry.";
RL   Electrophoresis 17:866-876(1996).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC       FORMED BY THE REMOVAL OF APPROXIMATELY 24 RESIDUES FROM THE
CC       CARBOXYL END.
CC   -!- POLYMORPHISM: BOTH SAA1 AND SAA2 HAVE A NUMBER OF ALLELES. WE USE
CC       HERE THE NOMENCLATURE OF REF.6. THE SEQUENCE SHOWN IS THAT OF
CC       1-ALPHA.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- DISEASE: BOL IS FROM A PATIENT WITH WALDENSTROM'S
CC       MACROGLOBULINEMIA.
CC   -!- DISEASE: JL IS FROM A PATIENT WITH ANKYLOSING SPONDYLITIS.
CC   -!- DISEASE: TH IS FROM A PATIENT WITH JUVENILE RHEUMATOID ARTHRITIS.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M10906; AAA60297.1; -.
DR   EMBL; J03474; AAB59539.1; -.
DR   EMBL; M23698; AAA64799.1; -.
DR   EMBL; M23699; AAA64800.1; -.
DR   EMBL; M23700; AAA64801.1; -.
DR   EMBL; M26152; AAA85338.1; -.
DR   EMBL; BC007022; AAH07022.1; -.
DR   EMBL; BC020795; AAH20795.1; -.
DR   EMBL; X51439; CAA35804.1; -.

  Query Match           100.0%;  Score 77;  DB 1;  Length 122;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
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Db        110 PNHFRPAGLPEKY 122
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RESULT 3
SAA_BOVIN
ID   SAA_BOVIN      STANDARD;      PRT;   112 AA.
AC   P35541;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Serum amyloid A protein (SAA) [Contains: Amyloid protein A (Amyloid
DE   fibril protein AA)].
GN   SAA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=92150985; PubMed=1738817;
RA   Rossevatin K., Andresen P.K., Sletten K., Husebekk A., Husby G.,
RA   Nordstoga K., Johnson K.H., Westermark G.T., Westermark P.;
RT   "The complete amino acid sequence of bovine serum amyloid protein A
RT   (SAA) and of subspecies of the tissue-deposited amyloid fibril
RT   protein A.";
RL   Scand. J. Immunol. 35:217-224(1992).
RN   [2]
RP   SEQUENCE OF 1-90.
RX   MEDLINE=89080450; PubMed=2909653;
RA   Benson M.D., Dibartola S.P., Dwulet F.E.;
RT   "A unique insertion in the primary structure of bovine amyloid AA
RT   protein.";
RL   J. Lab. Clin. Med. 113:67-72(1989).
RN   [3]
RP   SEQUENCE OF 4-16.
RX   MEDLINE=88277778; PubMed=3393848;
RA   Husebekk A., Husby G., Sletten K., Skogen B., Nordstoga K.;
RT   "Characterization of bovine amyloid proteins SAA and AA.";
RL   Scand. J. Immunol. 27:739-743(1988).
RN   [4]
RP   SEQUENCE OF 3-48.
RX   MEDLINE=87079535; PubMed=3791962;
RA   Westermark P., Johnson K.H., Westermark G.T., Sletten K., Hayden D.W.;
RT   "Bovine amyloid protein AA: isolation and amino acid sequence
RT   analysis.";
RL   Comp. Biochem. Physiol. 85B:609-614(1986).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC       FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; Plasma; HDL; Amyloid; Pyrrolidone carboxylic acid.
FT   CHAIN         1    112       SERUM AMYLOID A PROTEIN.
FT   CHAIN         1     90       AMYLOID PROTEIN A.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   112 AA;  12603 MW;  66E88810D4D49D34 CRC64;

  Query Match            96.1%;  Score 74;  DB 1;  Length 112;
  Best Local Similarity  92.3%;  Pred. No. 6.6e-06;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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RX   MEDLINE=86250747; PubMed=3013853;
RA   Lowell C.A., Potter D.A., Stearman R.S., Morrow J.F.;
RT   "Structure of the murine serum amyloid A gene family. Gene
RT   conversion.";
RL   J. Biol. Chem. 261:8442-8452(1986).
RN   [3]
RP   SEQUENCE OF 27-64 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=82229376; PubMed=6953913;
RA   Stearman R.S., Lowell C.A., Pearson W.R., Morrow J.F.;
RT   "Regulation of synthesis of amyloid A-related protein.";
RL   Ann. N.Y. Acad. Sci. 389:106-115(1982).
RN   [4]
RP   SEQUENCE OF 32-122 FROM N.A.
RX   MEDLINE=87309776; PubMed=3624868;
RA   Yamamoto K.I., Goto N., Kosaka J., Shiroo M., Yeul Y.D., Migita S.;
RT   "Structural diversity of murine serum amyloid A genes. Evolutionary
RT   implications.";
RL   J. Immunol. 139:1683-1688(1987).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03479; CAA27199.1; -.
DR   EMBL; X03505; CAA27219.1; -.
DR   EMBL; X03506; CAA27219.1; JOINED.
DR   EMBL; X03507; CAA27219.1; JOINED.
DR   EMBL; M25467; AAA37231.1; -.
DR   EMBL; M17792; AAA40088.1; -.
DR   PIR; A23521; A23521.
DR   PIR; I71950; I71950.
DR   MGD; MGI:98223; Saa3.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; Plasma; HDL; Signal; Multigene family.
FT   SIGNAL       1     19
FT   CHAIN       20    122       SERUM AMYLOID A-3 PROTEIN.
FT   CONFLICT     57     57       R -> G (IN REF. 4).
SQ   SEQUENCE   122 AA;  13773 MW;  B9435F82D1B0B705 CRC64;

  Query Match             90.9%;  Score 70;  DB 1;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 3.6e-05;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||||||::|
Db        110 PNHFRPAGLPKRY 122


RESULT 9
SAA_SHEEP
ID   SAA_SHEEP      STANDARD;      PRT;   112 AA.
AC   P42819;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Serum amyloid A protein (SAA).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=94120345; PubMed=8290897;
RA   Syversen P.V., Juul J., Marhaug G., Husby G., Sletten K.;
RT   "The primary structure of serum amyloid A protein in the sheep:
RT   comparison with serum amyloid A in other species.";
RL   Scand. J. Immunol. 39:88-94(1994).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; Plasma; HDL; Amyloid; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   112 AA;  12688 MW;  11A37FD59A8C1649 CRC64;

  Query Match             89.6%;  Score 69;  DB 1;  Length 112;
  Best Local Similarity   84.6%;  Pred. No. 4.9e-05;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||:|||:||
Db        100 PNHFRPPGLPDKY 112


RESULT 10
SAA1_RABIT
ID   SAA1_RABIT     STANDARD;      PRT;   122 AA.
AC   P53614;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Serum amyloid A-1 protein precursor.
GN   SAA1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92086827; PubMed=1721234;
RA   Rygg M., Marhaug G., Husby G., Dowton S.B.;
RT   "Rabbit serum amyloid protein A: expression and primary structure
RT   deduced from cDNA sequences.";
RL   Scand. J. Immunol. 34:727-734(1991).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S71722; AAB20616.1; -.
DR   PIR; I46981; I46981.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    122       SERUM AMYLOID A-1 PROTEIN.
SQ   SEQUENCE   122 AA;  13655 MW;  98822631B36B2B98 CRC64;

  Query Match             89.6%;  Score 69;  DB 1;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 5.3e-05;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db        110 PNHFRPKGLPDKY 122


RESULT 11
SAA2_RABIT
ID   SAA2_RABIT     STANDARD;      PRT;   122 AA.
AC   P22000;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Serum amyloid A-2 protein precursor.
GN   SAA2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91081342; PubMed=2259638;
RA   Tatum F., Alam J., Smith A., Morgan W.T.;
RT   "Molecular cloning, nucleotide sequence heterozygosity and regulation
RT   of rabbit serum amyloid A cDNA.";
RL   Nucleic Acids Res. 18:7447-7447(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91298985; PubMed=1712590;
RA   Ray B.K., Ray A.;
RT   "Complementary DNA cloning and nucleotide sequence of rabbit serum
RT   amyloid A protein.";
RL   Biochem. Biophys. Res. Commun. 178:68-72(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92086827; PubMed=1721234;
RA   Rygg M., Marhaug G., Husby G., Dowton S.B.;
RT   "Rabbit serum amyloid protein A: expression and primary structure
RT   deduced from cDNA sequences.";
RL   Scand. J. Immunol. 34:727-734(1991).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC   ----------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X16428; CAA34451.1; -.
DR   EMBL; X16427; CAA34450.1; -.
DR   EMBL; S71725; AAB20617.1; -.
DR   PIR; I46982; I46982.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
FT   SIGNAL       1     19
FT   CHAIN       20    122       SERUM AMYLOID A-2 PROTEIN.
FT   VARIANT     96     96       A -> D.
FT   CONFLICT    40     40       S -> T (IN REF. 2).
SQ   SEQUENCE   122 AA;  13451 MW;  C135BEE727C57C15 CRC64;

  Query Match             89.6%;  Score 69;  DB 1;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 5.3e-05;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||| |||:||
Db        110 PNHFRPKGLPDKY 122


RESULT 12
SAA3_RABIT
ID   SAA3_RABIT     STANDARD;      PRT;   122 AA.
AC   P35543;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Serum amyloid A-3 protein precursor.
GN   SAA3.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91185595; PubMed=1849144;
RA   Mitchell T.I., Coon C.I., Brinckerhoff C.E.;
RT   "Serum amyloid A (SAA3) produced by rabbit synovial fibroblasts
RT   treated with phorbol esters or interleukin 1 induces synthesis of
RT   collagenase and is neutralized with specific antiserum.";
RL   J. Clin. Invest. 87:1177-1185(1991).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- INDUCTION: Upon cytokine stimulation.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M64696; AAA31464.1; -.
DR   PIR; S32574; S32574.
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OM protein - protein search, using sw model

Run on: August 18, 2003, 01:10:58 ; Search time 67 Seconds
(without alignments)
50.070 Million cell updates/sec

Title: US-09-846-779-1
Perfect score: 77
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

otal number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	122	4	Q16834	Q16834 homo sapien
2	74	96.1	131	6	Q8SQ28	Q8sq28 bos taurus
3	69	89.6	122	6	Q29514	Q29514 oryctolagus
4	68	88.3	128	6	Q9N0Y1	Q9n0y1 equus cabal
5	67	87.0	143	6	Q9MZT5	Q9mzt5 bos taurus
6	67	87.0	159	11	Q64423	Q64423 mesocricetu
7	66	85.7	111	6	Q9XSG7	Q9xsg7 felis silve
8	60	77.9	122	11	Q8R3T4	Q8r3t4 mus musculu
9	60	77.9	122	11	Q64454	Q64454 mus musculu
10	60	77.9	122	11	P97374	P97374 mus musculu
11	60	77.9	122	11	P97375	P97375 mus musculu
12	57	74.0	123	13	Q9YIA4	Q9yia4 cyprinus ca
13	55	71.4	114	13	P79900	P79900 oncorhynchu
14	55	71.4	127	5	Q8MY11	Q8my11 branchiosto
15	53	68.8	122	5	Q9GSP8	Q9gsp8 holothuria
16	52	67.5	129	13	Q8JIB0	Q8jib0 sphenodon p
17	47	61.0	355	10	Q9AUL4	Q9aul4 oryza sativ
18	46	59.7	404	10	Q8L9L1	Q81911 arabidopsis
19	46	59.7	404	10	Q9LYB3	Q9lyb3 arabidopsis
20	46	59.7	1347	5	Q95WR8	Q95wr8 caenorhabdi
21	46	59.7	1470	5	Q21218	Q21218 caenorhabdi
22	45	58.4	88	5	Q9TWA9	Q9twa9 drosophila
23	45	58.4	2329	5	Q8IG47	Q8ig47 caenorhabdi
24	45	58.4	2747	5	Q8IG48	Q8ig48 caenorhabdi
25	44	57.1	364	16	Q9PEG1	Q9peg1 xylella fas
26	44	57.1	921	11	Q8BSQ4	Q8bsq4 mus musculu
27	43.5	56.5	514	8	Q95938	Q95938 rattus norv
28	43	55.8	306	2	Q93GX6	Q93gx6 streptomyce
29	42	54.5	123	11	Q61243	Q61243 mus musculu
30	42	54.5	737	3	Q9HDE9	Q9hde9 metarhizium
31	41	53.2	145	16	Q9JWF9	Q9jwf9 neisseria m
32	41	53.2	152	16	Q9JXH6	Q9jxh6 neisseria m
33	41	53.2	187	6	Q95L50	Q95150 bos taurus
34	41	53.2	205	16	Q8KAA5	Q8kaa5 chlorobium
35	41	53.2	413	1	O93709	O93709 sulfolobus
36	41	53.2	414	17	Q97WY1	Q97wy1 sulfolobus
37	41	53.2	429	2	Q8GAH1	Q8gah1 arthrobacte
38	41	53.2	430	2	O31226	O31226 arthrobacte
39	41	53.2	595	5	Q9W362	Q9w362 drosophila
40	41	53.2	622	10	Q9LWK7	Q9lwk7 oryza sativ
41	41	53.2	649	16	Q8FG07	Q8fg07 escherichia
42	40.5	52.6	464	10	O48967	O48967 zea mays (m
43	40	51.9	137	2	Q9F907	Q9f907 treponema p
44	40	51.9	229	16	Q8PM20	Q8pm20 xanthomonas
45	40	51.9	233	4	Q96I69	Q96i69 homo sapien

ALIGNMENTS

RESULT 1
Q16834
ID Q16834 PRELIMINARY; PRT; 122 AA.
AC Q16834;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SAAB1 beta protein precursor (Serum amyloid A protein).
GN SAAB1 BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92022342; PubMed=1656519;
RA Betts J.C., Edbrooke M.R., Thakker R.V., Woo P.;
RT "The human acute-phase serum amyloid A gene family: structure,
RT evolution and expression in hepatoma cells.";
RL Scand. J. Immunol. 34:471-482(1991).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; X56652; CAA39974.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 122 POTENTIAL.
SQ SEQUENCE 122 AA; 13532 MW; D913BF06AA4107A2 CRC64;

Query Match 100.0%; Score 77; DB 4; Length 122;

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  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||||||||||||
Db        110 PNHFRPAGLPEKY 122


RESULT 2
Q8SQ28
ID   Q8SQ28      PRELIMINARY;      PRT;   131 AA.
AC   Q8SQ28;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Serum amyloid A3 isoform protein precursor (Serum amyloid A
DE   protein).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21589074; PubMed=11730930;
RA   McDonald T.L., Larson M.A., Mack D.R., Weber A.;
RT   "Elevated extrahepatic expression and secretion of mammary-associated
RT   serum amyloid A 3 (M-SAA3) into colostrum.";
RL   Vet. Immunol. Immunopathol. 83:203-211(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gutierrez-Pabello J.A., Barthel R., Adams G.;
RT   "Differential gene expression of Mycobacterium bovis infected bovine
RT   macrophages.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; AF335552; AAM11538.1; -.
DR   EMBL; AF540564; AAN17326.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL; Signal.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    131       SERUM AMYLOID A3 ISOFORM PROTEIN.
SQ   SEQUENCE   131 AA;  14723 MW;  BB5F58F07A3B9331 CRC64;

  Query Match             96.1%;  Score 74;  DB 6;  Length 131;
  Best Local Similarity   92.3%;  Pred. No. 5.4e-05;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||||||:||
Db        119 PNHFRPAGLPDKY 131


RESULT 3
Q29514
ID   Q29514      PRELIMINARY;      PRT;   122 AA.
AC   Q29514;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical serum amyloid A protein.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91315474; PubMed=1859410;
RA   Ray B.K., Ray A.;
RT   "Molecular cloning and nucleotide sequence of complementary DNA
RT   encoding rabbit alpha 1-acid glycoprotein.";
RL   Biochem. Biophys. Res. Commun. 178:507-513(1991).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; X58728; CAA41560.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Hypothetical protein; Acute phase; HDL.
SQ   SEQUENCE   122 AA;  13509 MW;  B635BEB222907945 CRC64;

  Query Match             89.6%;  Score 69;  DB 6;  Length 122;
  Best Local Similarity   84.6%;  Pred. No. 0.00036;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||||||  |||:||
Db        110 PNHFRPKGLPDKY 122


RESULT 4
Q9N0Y1
ID   Q9N0Y1      PRELIMINARY;      PRT;   128 AA.
AC   Q9N0Y1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A precursor (Serum amyloid A protein).
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20579389; PubMed=11137129;
RA   Ma Z., Mizukoshi T., Khatlani T.S., Okuda M., Onishi T.;
RT   "Molecular cloning and sequencing of equine cDNA encoding serum
RT   amyloid A (SAA).";
RL   Vet. Immunol. Immunopathol. 77:321-327(2000).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; AF240364; AAF63164.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL; Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   128 AA;  14067 MW;  CA8F4DF1F1DD2A33 CRC64;

  Query Match             88.3%;  Score 68;  DB 6;  Length 128;
  Best Local Similarity   84.6%;  Pred. No. 0.00057;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
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              |||||| |||:||
Db        116 PNHFRPHGLPDKY 128


RESULT 5
Q9MZT5
ID   Q9MZT5      PRELIMINARY;      PRT;   143 AA.
AC   Q9MZT5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein.
GN   SAA3.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
 C   TISSUE=Mammary gland;
..A  Kho Y.J., Choi Y.J., Baik M.G.;
RT   "Cloning and characterization of involution-specific genes from the
RT   bovine mammary gland.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; AF160867; AAF77630.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   143 AA;  15819 MW;  F32DE20B5A635D2C CRC64;

  Query Match             87.0%;  Score 67;  DB 6;  Length 143;
  Best Local Similarity   91.7%;  Pred. No. 0.00094;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEK 12
              |||||||||||:|
Db        119 PNHFRPAGLPDK 130


.ESULT 6
.Q64423
ID   Q64423      PRELIMINARY;      PRT;   159 AA.
AC   Q64423;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein.
GN   SAA3.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89352552; PubMed=2765510;
RA   Webb C.F., Tucker P.W., Dowton S.B.;
RT   "Expression and sequence analysis of serum amyloid a in the Syrian
RT   hamster.";
RL   Biochemistry 28:4785-4790(1989).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; L13384; AAA37097.1; -.
DR   EMBL; M27241; AAA37097.1; JOINED.
DR   EMBL; L13383; AAA37097.1; JOINED.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   159 AA;  17955 MW;  8B4787705E9940A5 CRC64;

  Query Match             87.0%;  Score 67;  DB 11;  Length 159;
  Best Local Similarity   84.6%;  Pred. No. 0.0011;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |:||||||| ||
Db        147 PHHFRPAGLPSKY 159


RESULT 7
Q9XSG7
ID   Q9XSG7      PRELIMINARY;      PRT;   111 AA.
AC   Q9XSG7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein (Fragment).
GN   SAA.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ohno K., Terado M., Iwata H., Inokuma H., Onishi T.;
RT   "Expression of recombinant feline serum amyloid A (SAA) protein.";
RL   J. Vet. Med. Sci. 0:0-0(1999).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; AF136718; AAD24489.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
FT   NON_TER       1      1
SQ   SEQUENCE   111 AA;  12547 MW;  D9392BD358AF5D22 CRC64;

  Query Match             85.7%;  Score 66;  DB 6;  Length 111;
  Best Local Similarity   76.9%;  Pred. No. 0.0011;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              |||:|| |||:||
Db         99 PNHYRPEGLPDKY 111


RESULT 8
Q8R3T4
ID   Q8R3T4      PRELIMINARY;      PRT;   122 AA.
AC   Q8R3T4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
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DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to serum amyloid A 2 (Serum amyloid A protein).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; BC024606; AAH24606.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   122 AA;  13732 MW;  53F4A895D1DC15DB CRC64;

  Query Match             77.9%;  Score 60;  DB 11;  Length 122;
  Best Local Similarity   69.2%;  Pred. No. 0.013;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||::|| |||:||
Db        110 PNYYRPPGLPDKY 122


RESULT 9
Q64454
ID   Q64454      PRELIMINARY;      PRT;   122 AA.
AC   Q64454;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CE/J;
RX   MEDLINE=93388642; PubMed=8376413;
RA   de Beer M.C., de Beer F.C., McCubbin W.D., Kay C.M., Kindy M.S.;
RT   "Structural prerequisites for serum amyloid A fibril formation.";
RL   J. Biol. Chem. 268:20606-20612(1993).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; L22190; AAA19818.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   122 AA;  13700 MW;  FAA291682A8F770A CRC64;

  Query Match             77.9%;  Score 60;  DB 11;  Length 122;
  Best Local Similarity   69.2%;  Pred. No. 0.013;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||::|| |||:||
Db        110 PNYYRPPGLPQKY 122


RESULT 10
P97374
ID   P97374      PRELIMINARY;      PRT;   122 AA.
AC   P97374;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein isoform 1.
GN   SAA2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech;
RA   Cathcart E., Carreras I., Elliott-Bryant R., Liang J.S.,
RA   Gonnerman W.A., Sipe J.;
RT   "Polymorphisms of Acute Phase Serum Amyloid A Isoforms and Amyloid
RT   Resistence in Wild-type Mus musculus Czech.";
RL   Clin. Immunol. Immunopathol. 0:0-0(1996).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; U60437; AAB37249.1; -.
DR   MGD; MGI:98222; Saa2.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   122 AA;  13732 MW;  09EB8AA8C8E1B43E CRC64;

  Query Match             77.9%;  Score 60;  DB 11;  Length 122;
  Best Local Similarity   69.2%;  Pred. No. 0.013;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||::|| |||:||
Db        110 PNYYRPPGLPDKY 122


RESULT 11
P97375
ID   P97375      PRELIMINARY;      PRT;   122 AA.
AC   P97375;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein isoform 2.
GN   SAA2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech;
RA   Cathcart E., Carreras I., Elliott-Bryant R., Liang J.S.,
RA   Gonnerman W.S., Sipe J.;
RT   "Polymorphism of Acute Phase Serum Amyloid A Isoforms and Amyloid
RT   Resistence in Wild-type Mus musculus Czech.";
RL   Clin. Immunol. Immunopathol. 0:0-0(1996).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
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CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; U60438; AAB37250.1; -.
DR   MGD; MGI:98222; Saa2.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   122 AA;  13638 MW;  EEE79A1FE0432022 CRC64;

  Query Match             77.9%;  Score 60;  DB 11;  Length 122;
  Best Local Similarity   69.2%;  Pred. No. 0.013;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              ||::|| |||:||
Db        110 PNYYRPPGLPDKY 122


RESULT 12
Q9YIA4
ID   Q9YIA4      PRELIMINARY;      PRT;   123 AA.
AC   Q9YIA4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20394649; PubMed=10938736;
RA   Fujiki K., Shin D.H., Nakao M., Yano T.;
RT   "Molecular cloning and expression analysis of carp (Cyprinus carpio)
RT   interleukin-1beta, high affinity immunoglobulin E Fc receptor gamma
RT   subunit and serum amyloid A.";
RL   Fish and Shellfish Immunol. 10:229-242(2000).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; AB016524; BAA36700.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL.
SQ   SEQUENCE   123 AA;  13777 MW;  B364917D3B2C4B8A CRC64;

  Query Match             74.0%;  Score 57;  DB 13;  Length 123;
  Best Local Similarity   69.2%;  Pred. No. 0.042;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              || :|| |||:||
Db        111 PNRYRPRGLPKKY 123


RESULT 13
P79900
ID   P79900      PRELIMINARY;      PRT;   114 AA.
AC   P79900;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Acute phase serum amyloid A (SAA) precursor (Serum amyloid A protein)
DE   (Fragment).
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=97131713; PubMed=8977214;
RA   Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
RA   Whitehead A.S.;
RT   "Acute phase proteins in Salmonids. Evolutionary analyses and acute
RT   phase response.";
RL   J. Immunol. 158:384-392(1997).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR   EMBL; X99387; CAA67766.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
KW   Acute phase; HDL; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     11       POTENTIAL.
FT   CHAIN        12    114       ACUTE PHASE SERUM AMYLOID A (SAA).
SQ   SEQUENCE   114 AA;  12693 MW;  02D96C6F2ABE232C CRC64;

  Query Match             71.4%;  Score 55;  DB 13;  Length 114;
  Best Local Similarity   69.2%;  Pred. No. 0.086;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              || ||| |||: |
Db        102 PNRFRPQGLPKNY 114


RESULT 14
Q8MY11
ID   Q8MY11      PRELIMINARY;      PRT;   127 AA.
AC   Q8MY11;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Amyloid protein A.
GN   AMPAA.
OS   Branchiostoma belcheri (Amphoxius).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7741;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kubokawa K.;
RT   "Characterization of amyloid protein A in amphioxus.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB079688; BAB97379.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
SQ   SEQUENCE   127 AA;  14114 MW;  9C69A8FD98ECCE2F CRC64;

  Query Match             71.4%;  Score 55;  DB 5;  Length 127;
  Best Local Similarity   61.5%;  Pred. No. 0.097;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 PNHFRPAGLPEKY 13
              || :|| |||::|
Db        115 PNRYRPEGLPDRY 127


RESULT 15
Q9GSP8
ID   Q9GSP8      PRELIMINARY;      PRT;   122 AA.
AC   Q9GSP8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Serum amyloid A protein.
OS   Holothuria glaberrima.
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Holothuroidea; Aspidochirotacea; Aspidochirotida; Holothuriidae;
OC   Holothuria.
OX   NCBI_TaxID=31192;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Santiago-Cardona P.G., Roig-Lopez J.L., Santiago C.L.,
RA   Garcia-Arraras J.E.;
RT   "Holothuroid serum amyloid A protein.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF300706; AAG24633.1; -.
DR   InterPro; IPR000096; Serum_amyloid_A.
DR   Pfam; PF00277; SAA_proteins; 1.
DR   PRINTS; PR00306; SERUMAMYLOID.
DR   ProDom; PD002112; Serum_amyloid_A; 1.
DR   SMART; SM00197; SAA; 1.
DR   PROSITE; PS00992; SAA; 1.
SQ   SEQUENCE   122 AA;  13580 MW;  740FCE6C8661FD8B CRC64;

  Query Match             68.8%;  Score 53;  DB 5;  Length 122;
  Best Local Similarity   69.2%;  Pred. No. 0.2;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PNHFRPAGLPEKY 13
              || :|| ||| ||
Db        110 PNVYRPPGLPSKY 122


Search completed: August 18, 2003, 01:26:21
Job time : 72 secs
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